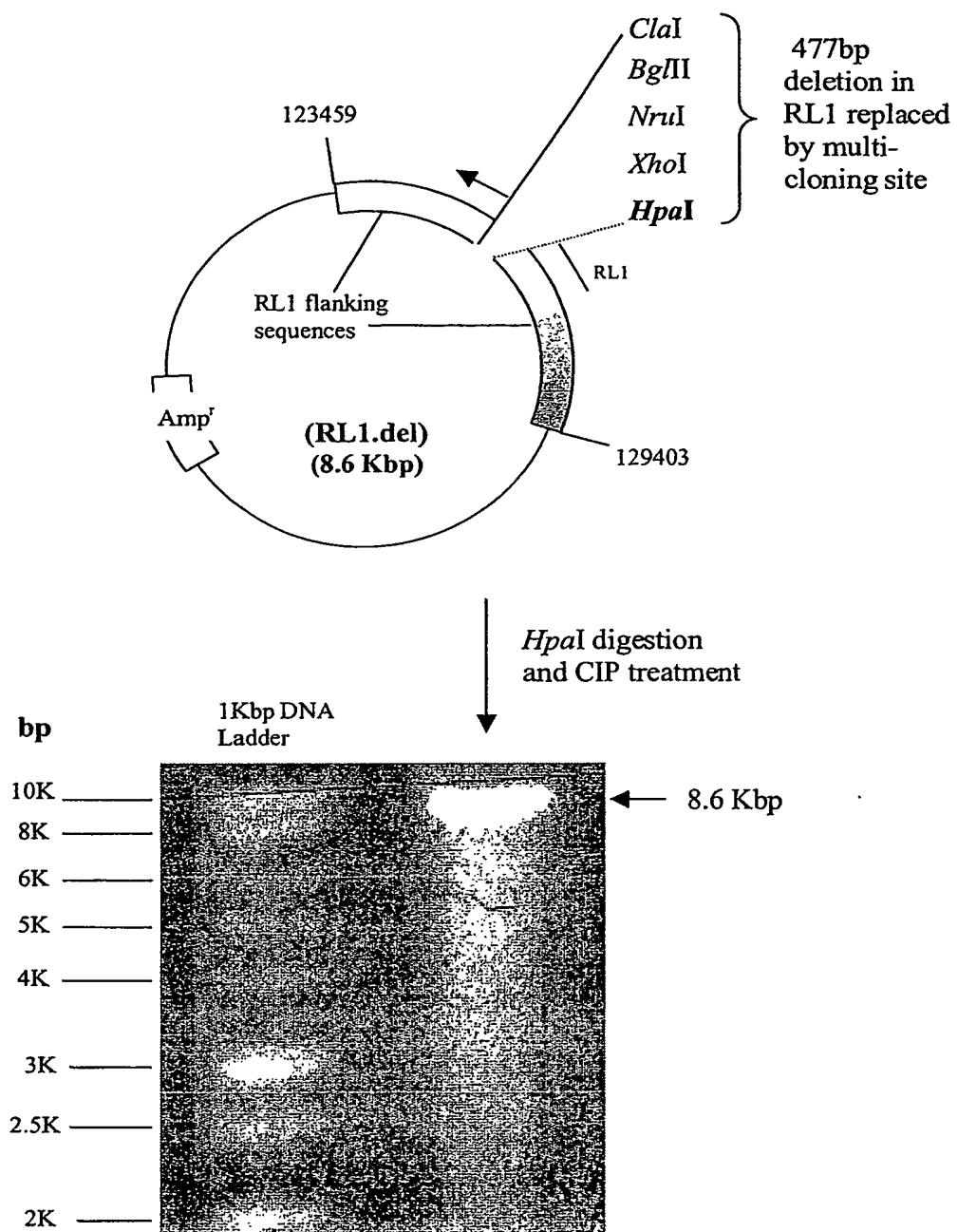
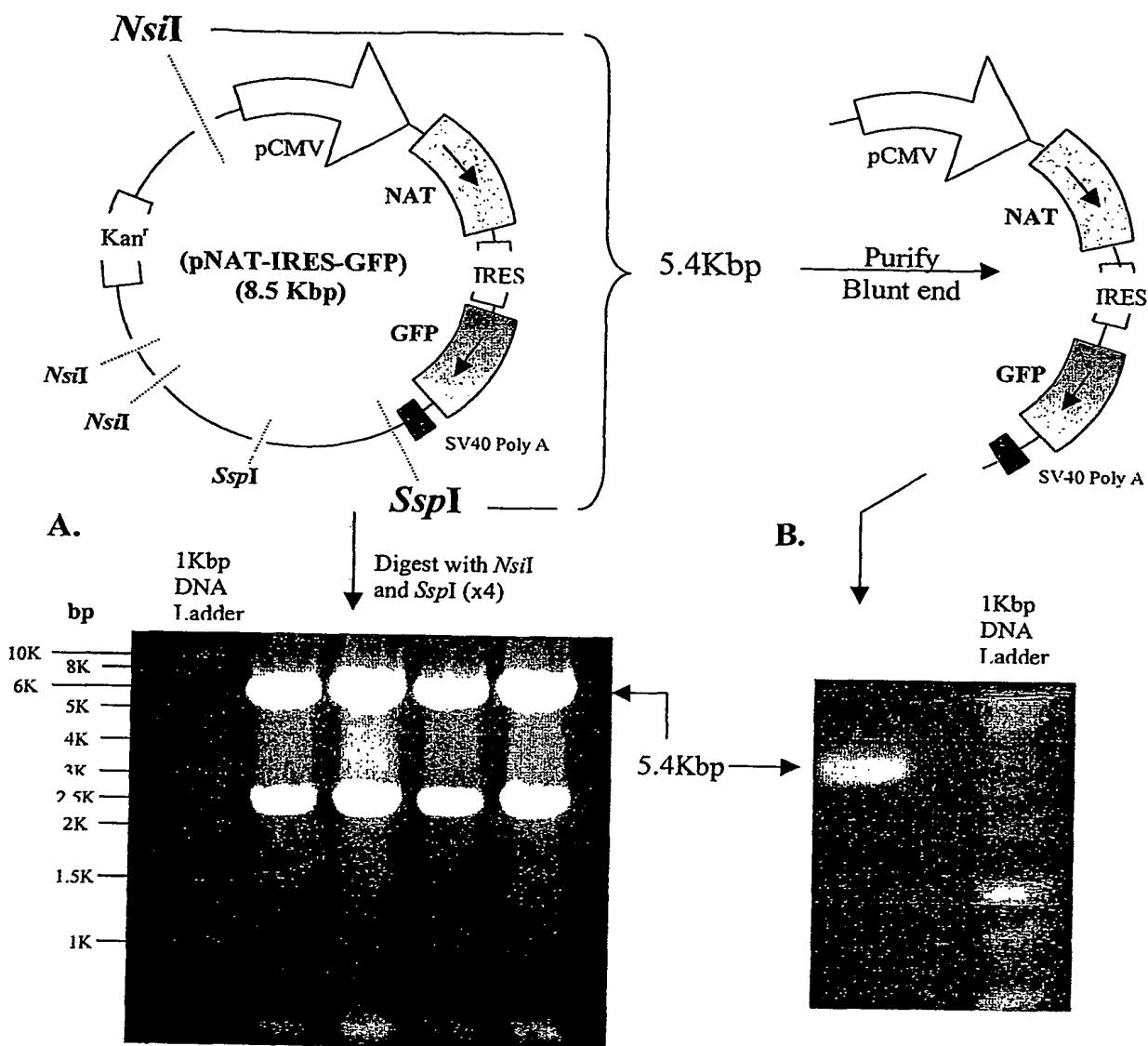
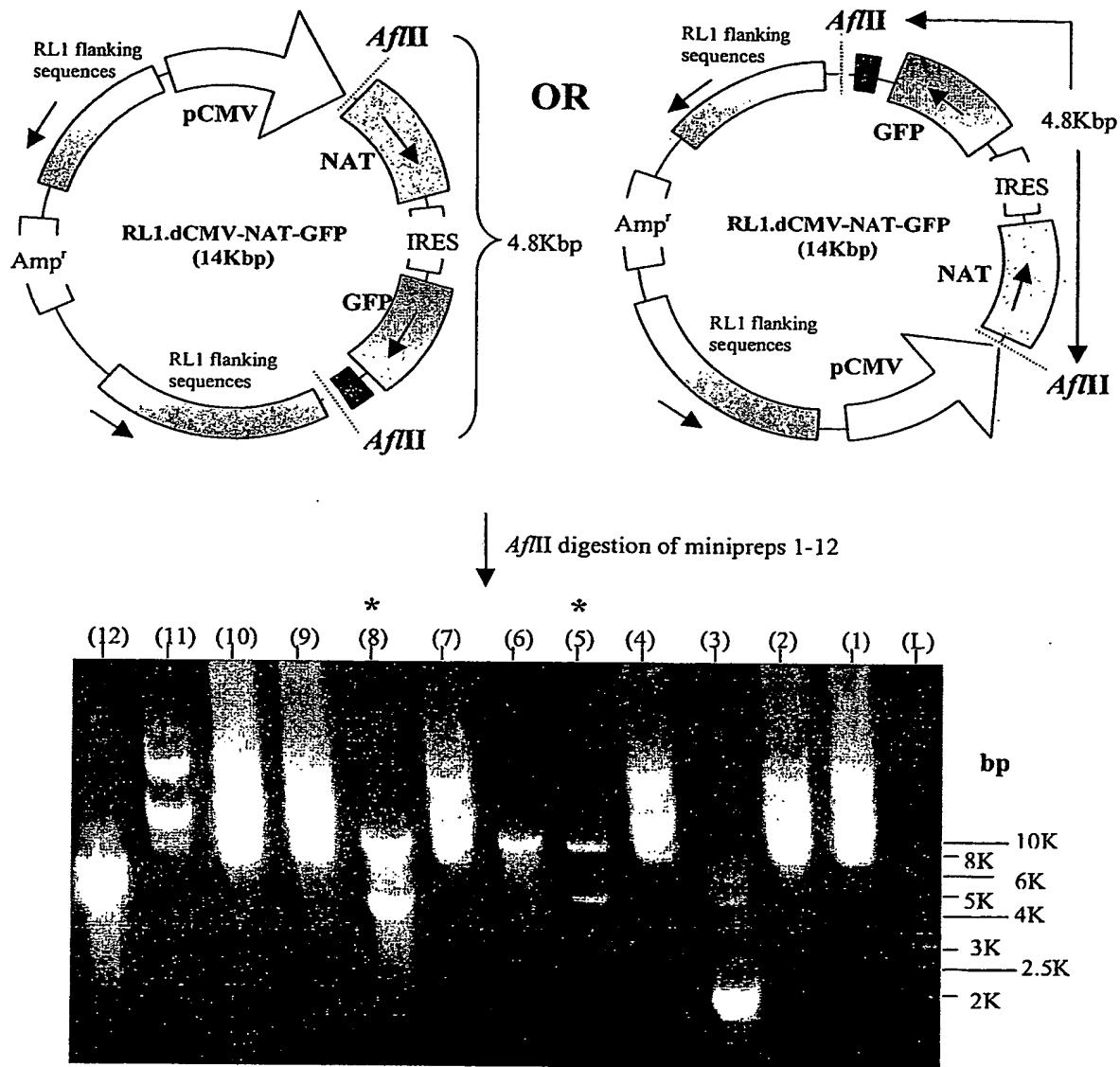


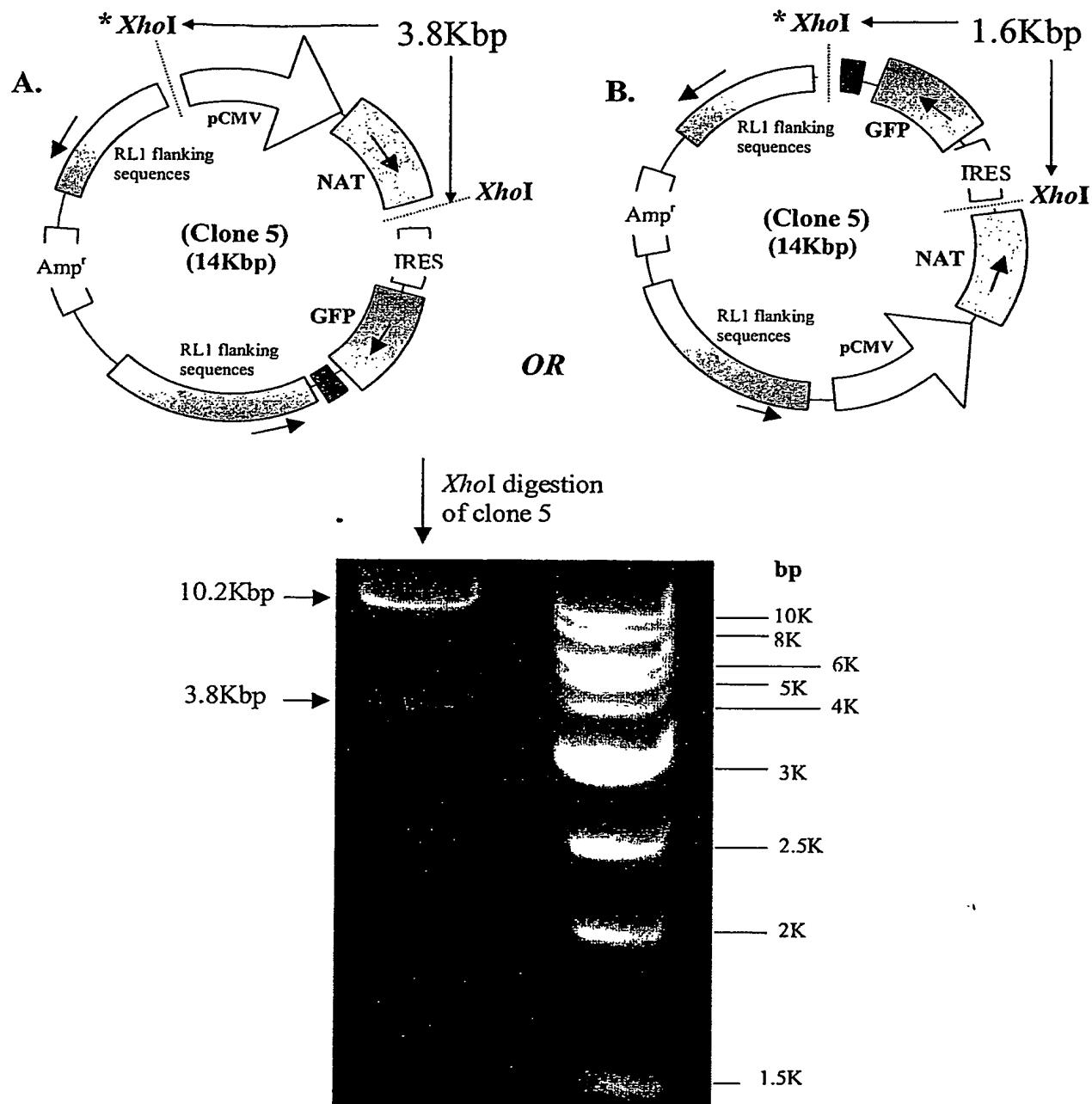
Figure 1

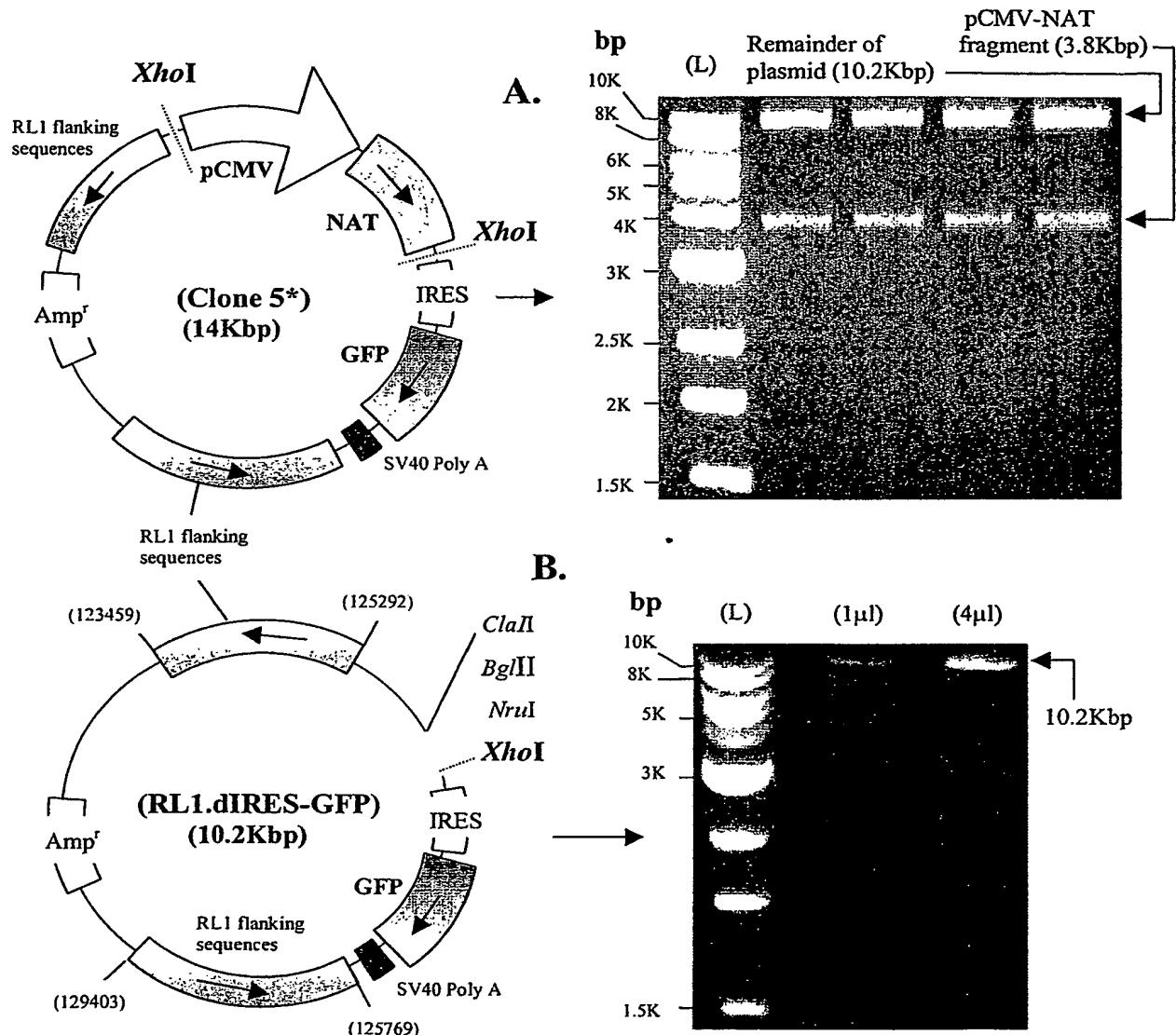
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**Figure 2**

**Figure 3**

**Figure 4**

**Figure 5**

**Figure 6**

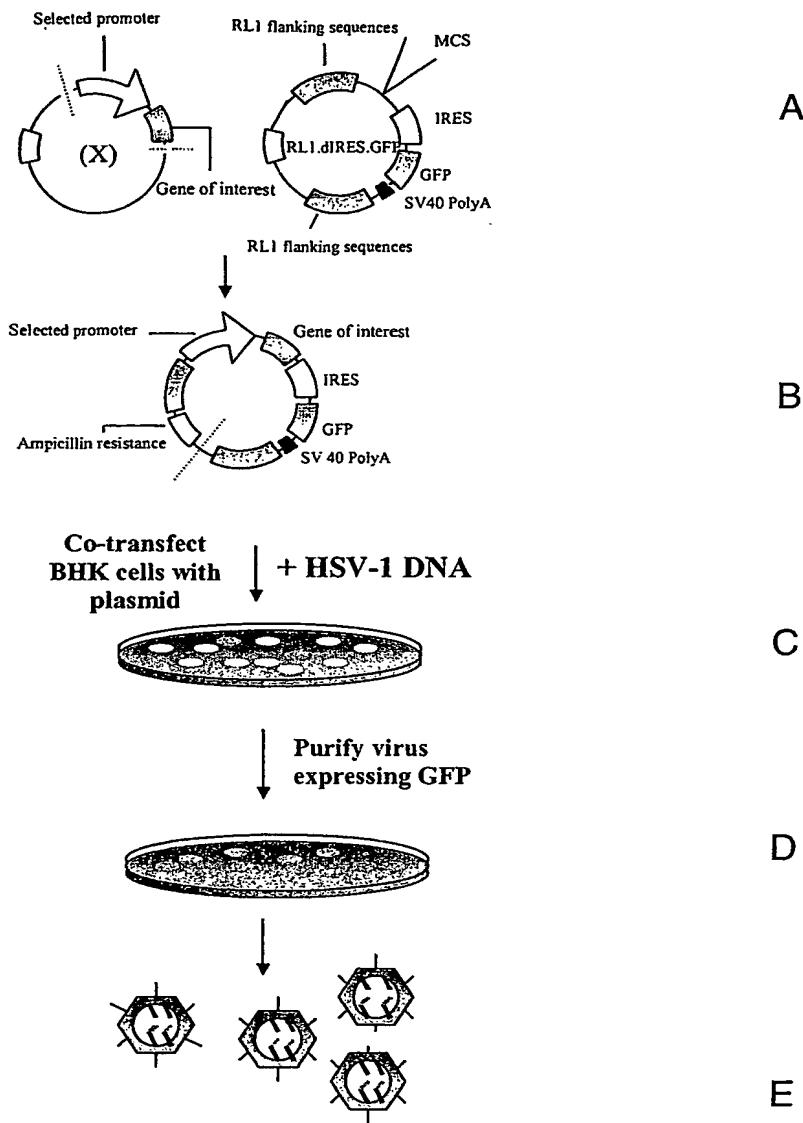
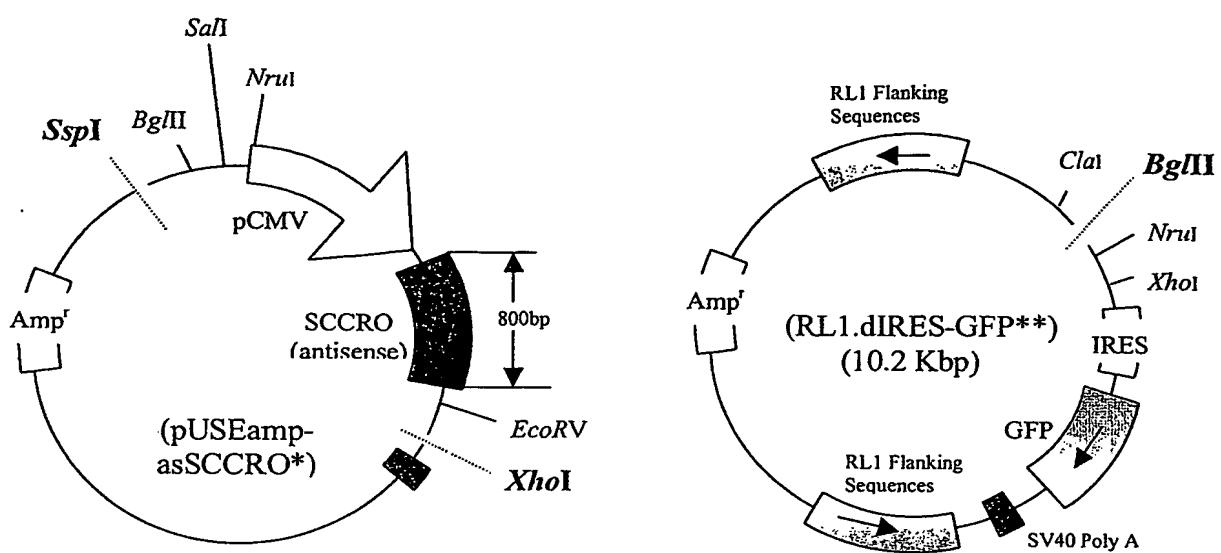


Figure 7



1. Digest with *Xba*I and *Ssp*I, purify and blunt end the 1.96Kbp fragment

2. Digest with *Bgl*II, blunt end and treat with CIP

3. Clone the blunt ended pCMV-asSCCRO into *Bgl*II digested/blunt ended/CIP treated RL1.dIRES-GFP

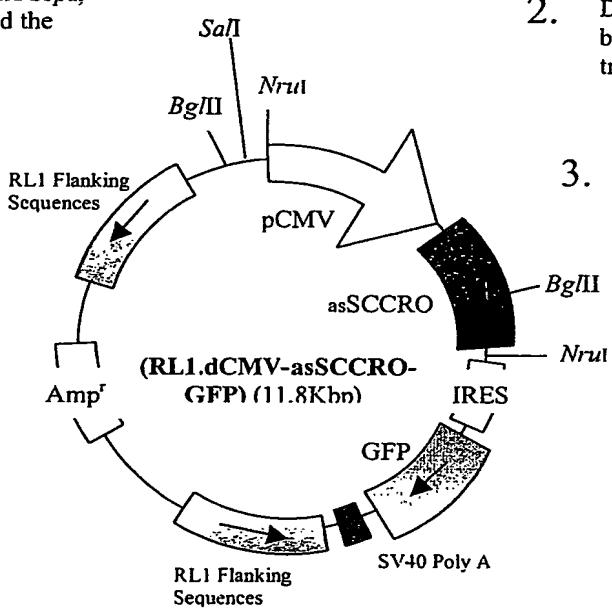


Figure 8

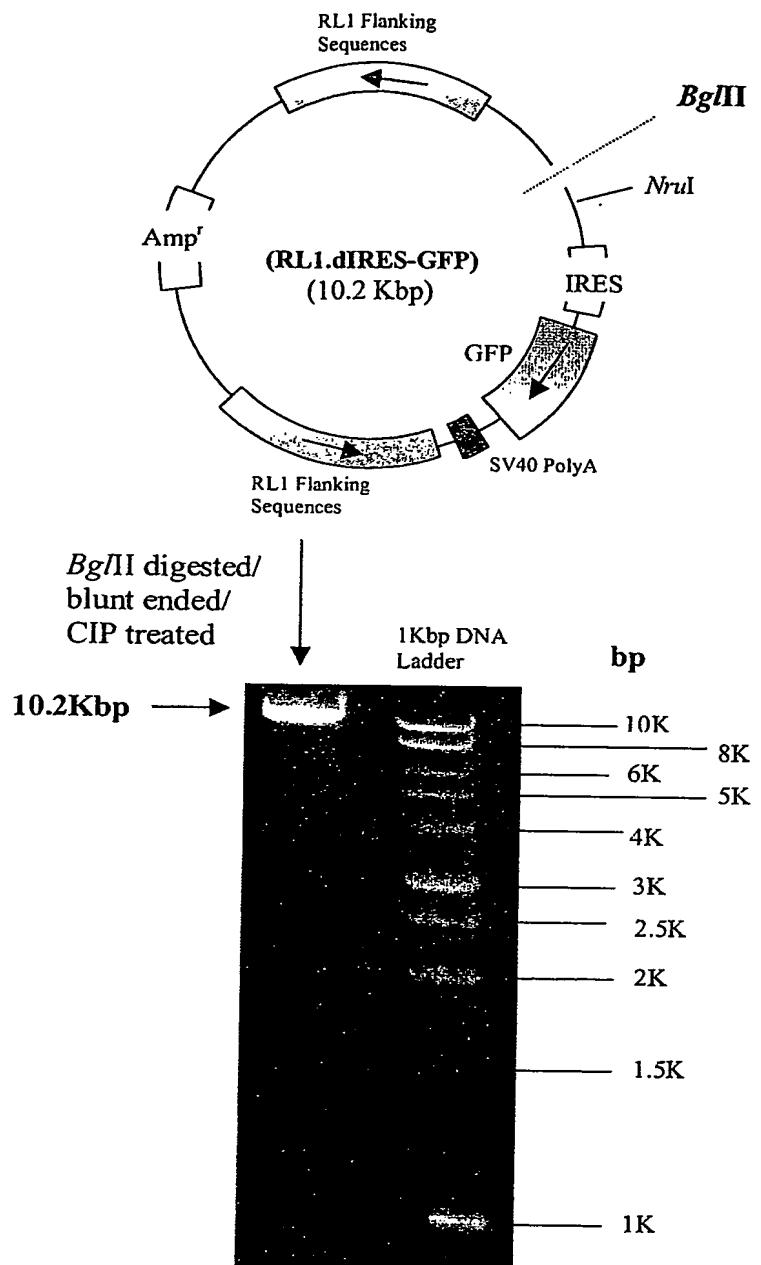
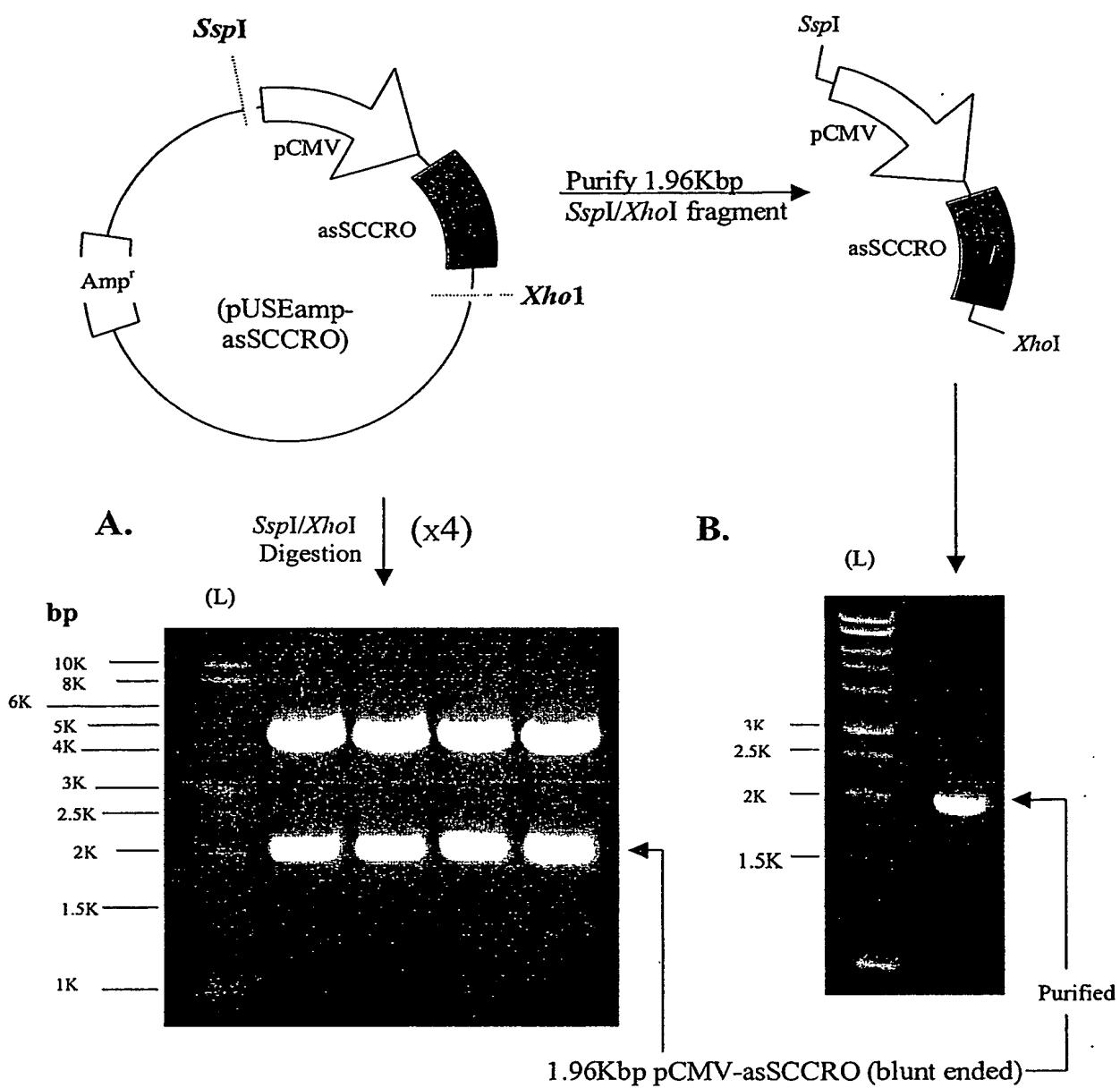
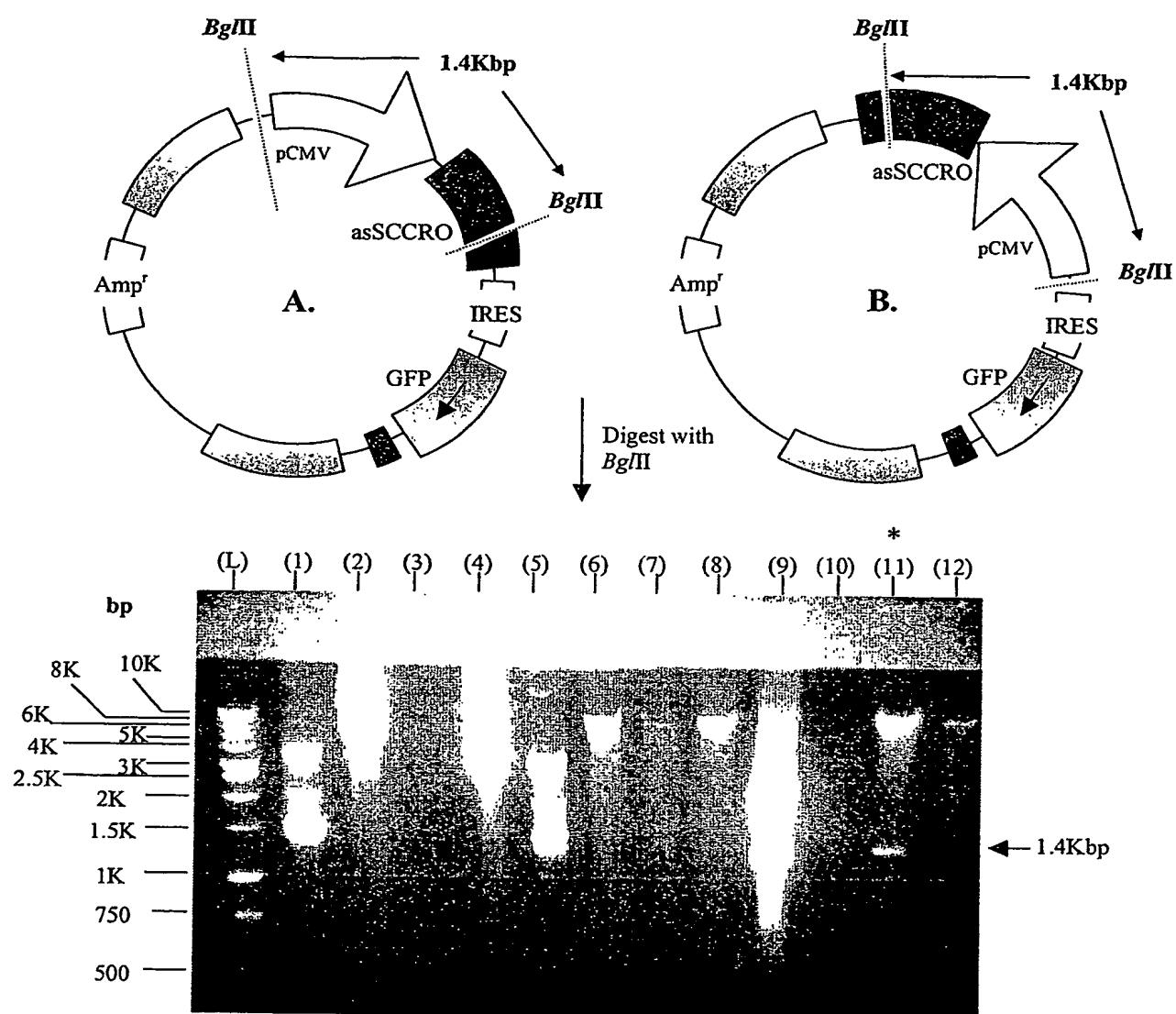
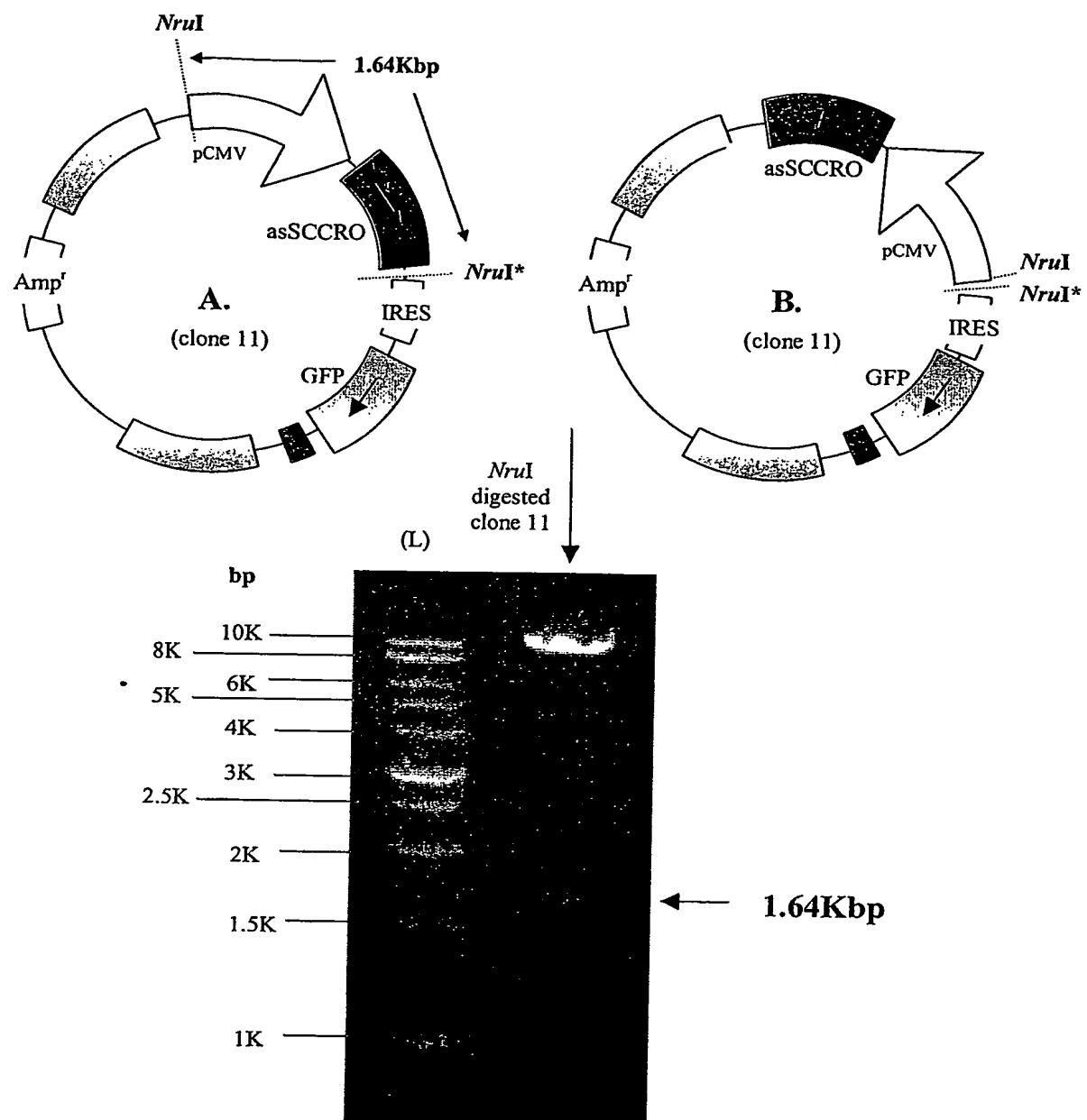
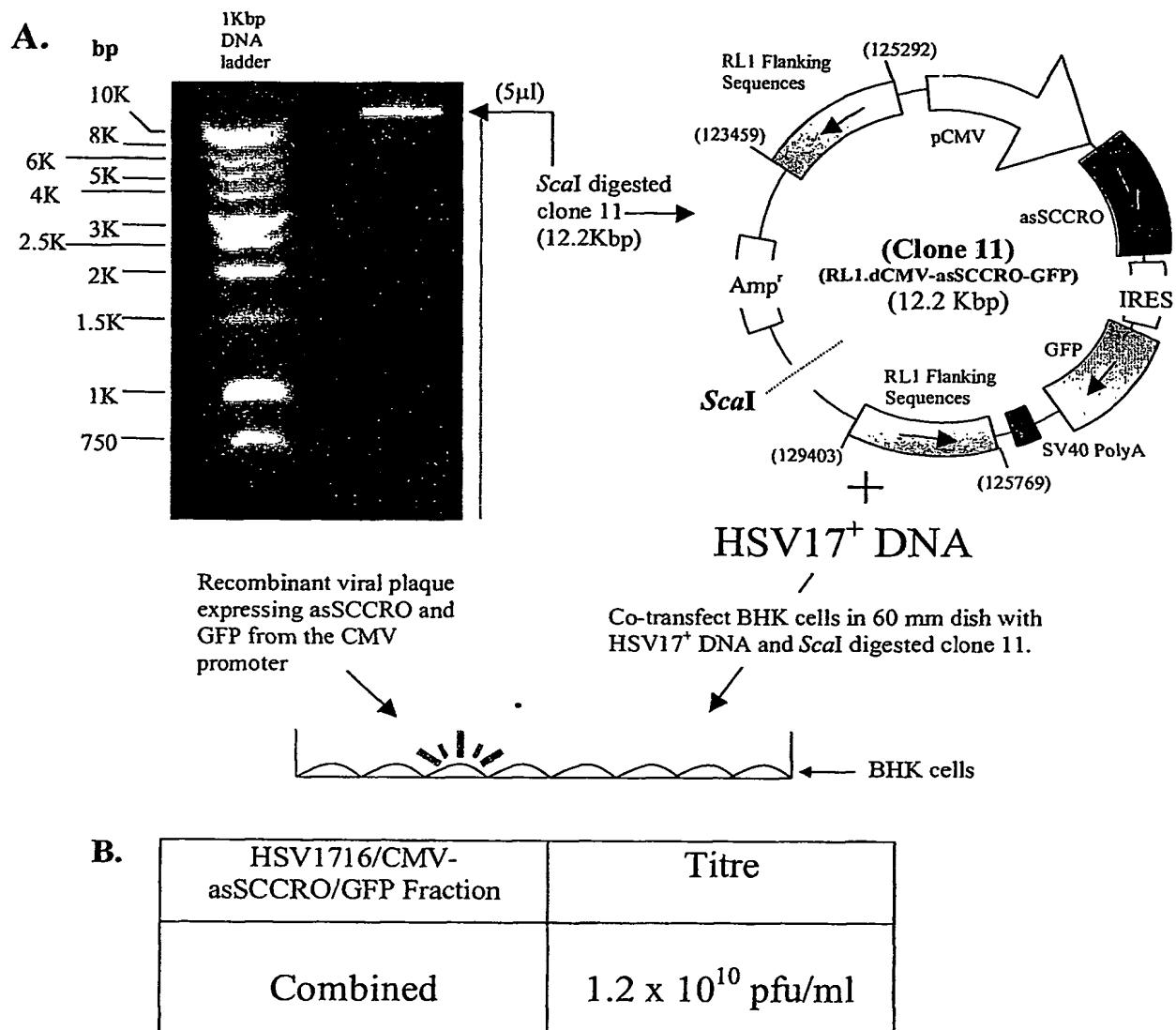


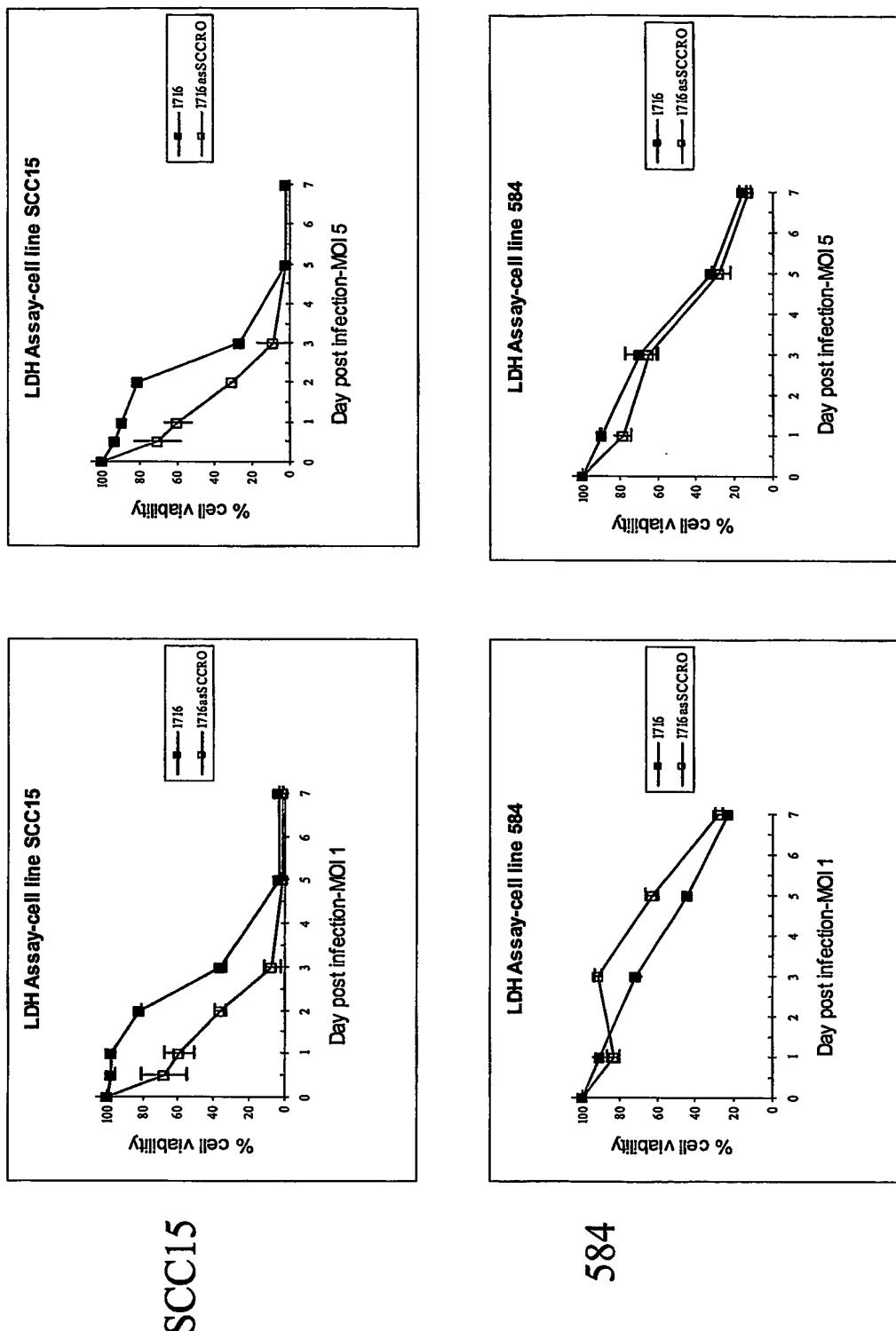
Figure 9

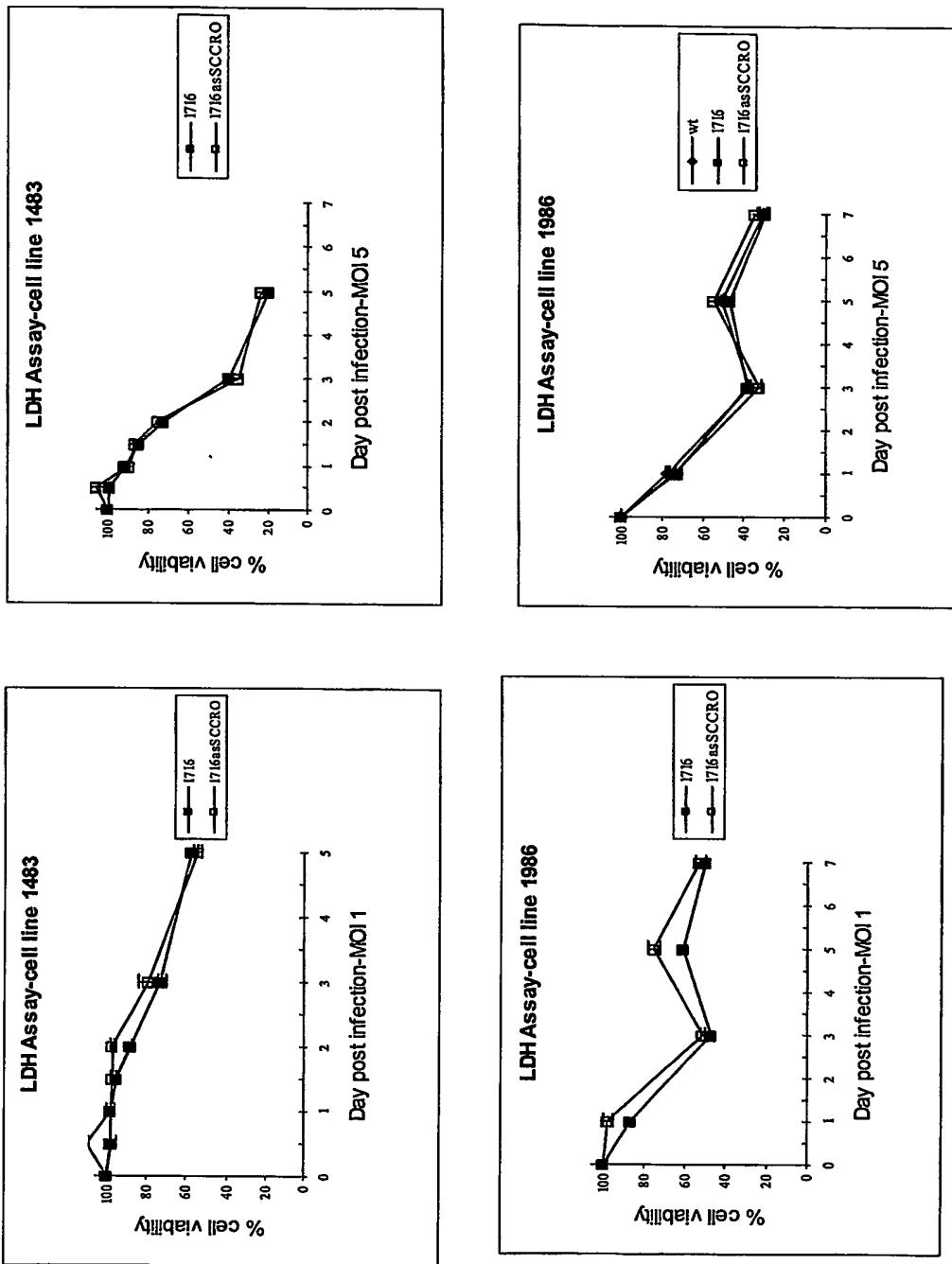
**Figure 10**

**Figure 11**

**Figure 12**

**Figure 13**

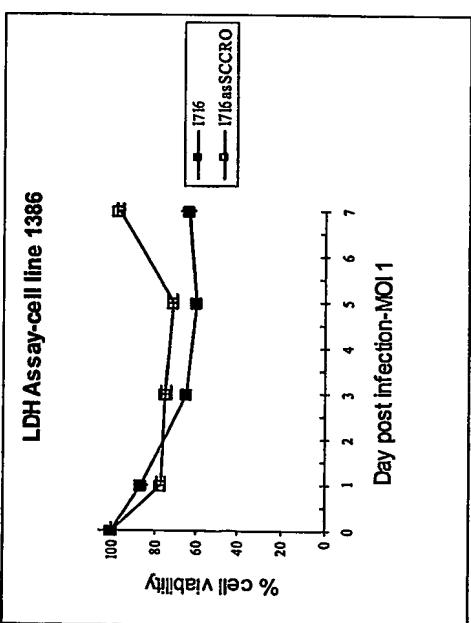
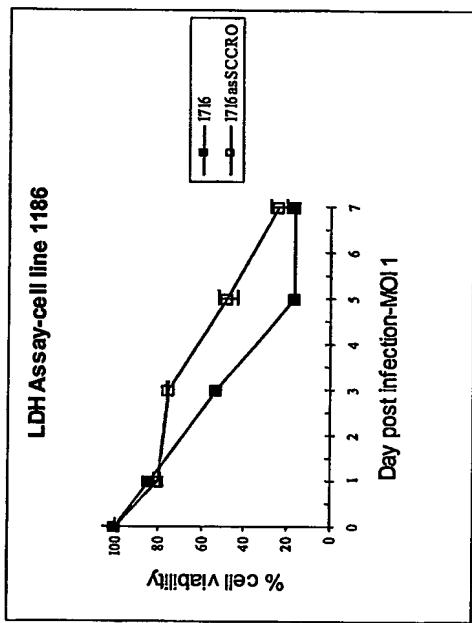
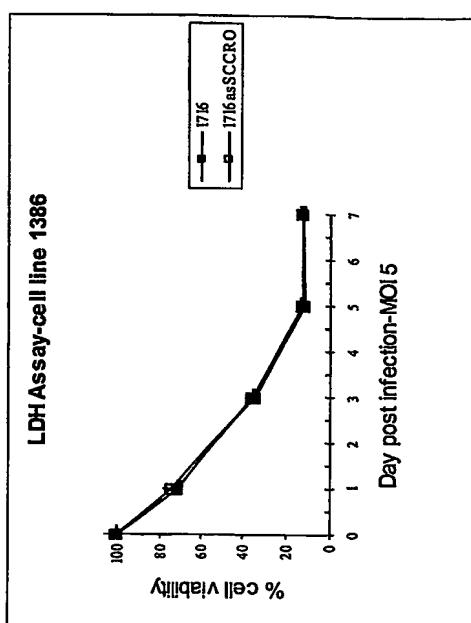
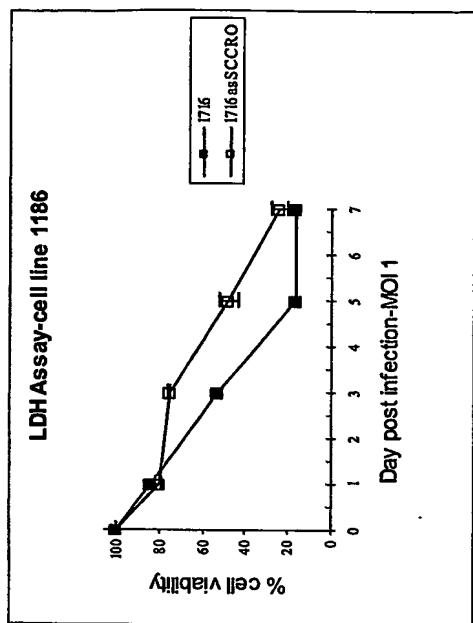
**Figure 14**



1483

1986

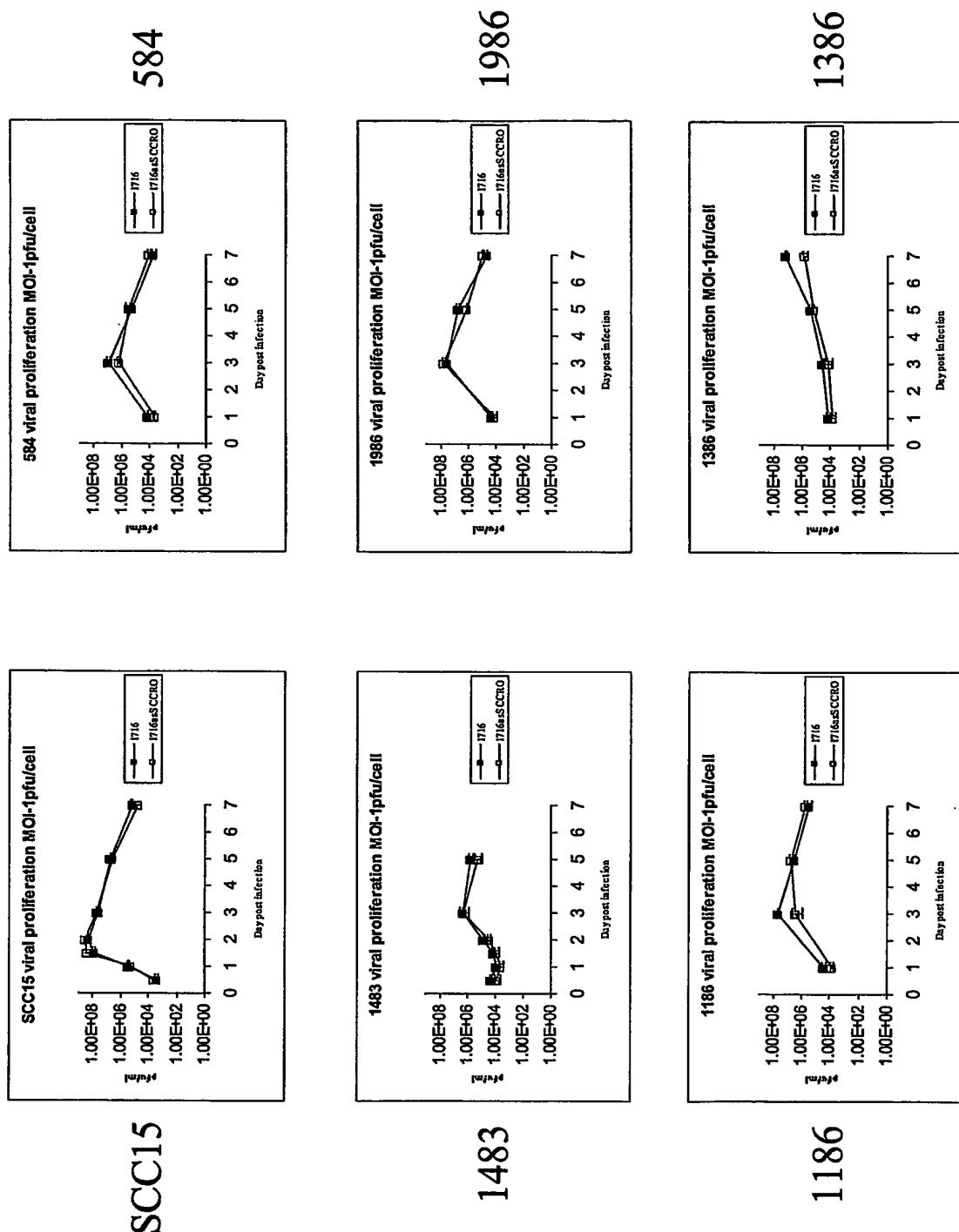
Figure 15



1186

1386

Figure 16

**Figure 17**

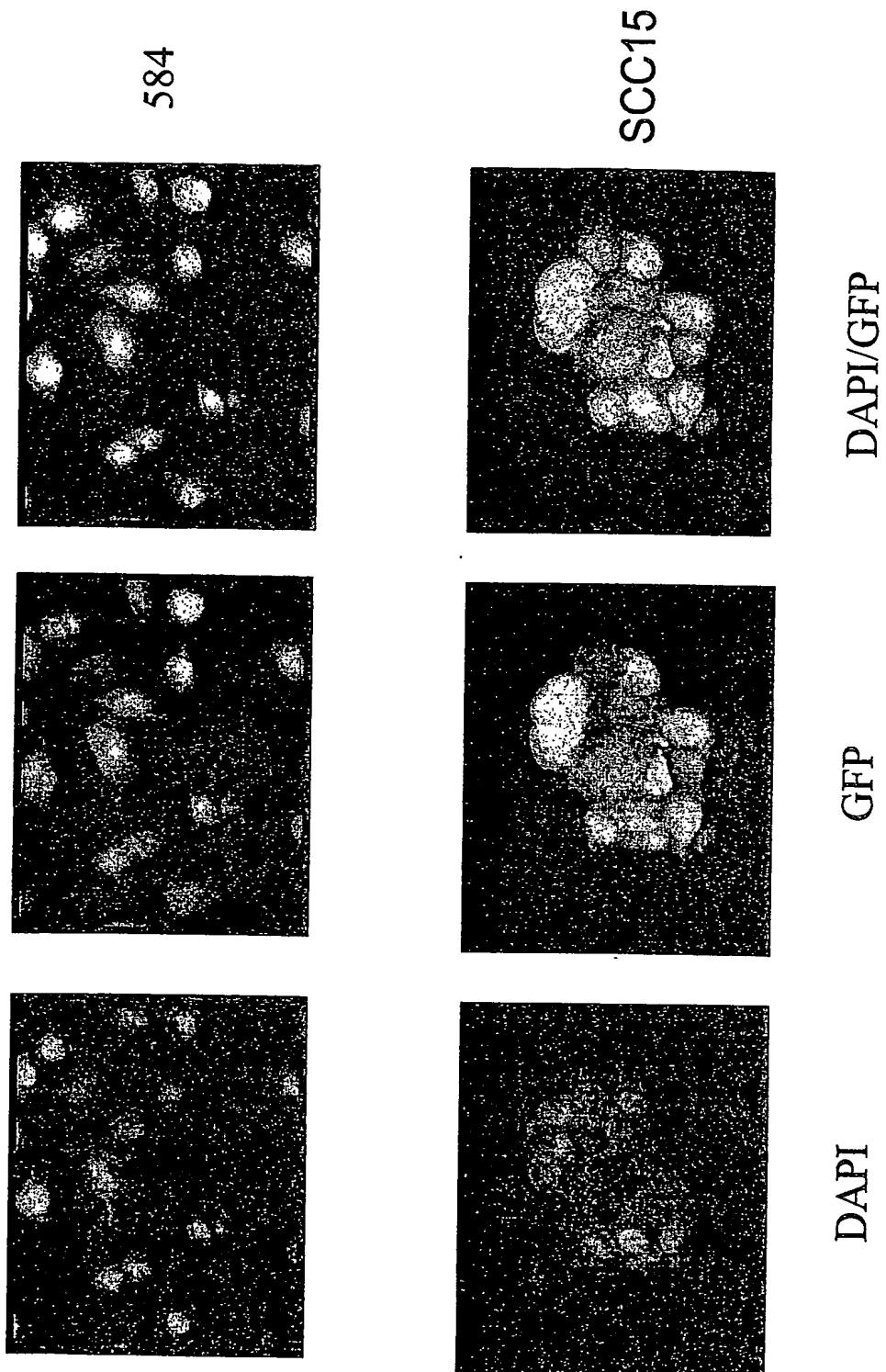


Figure 18

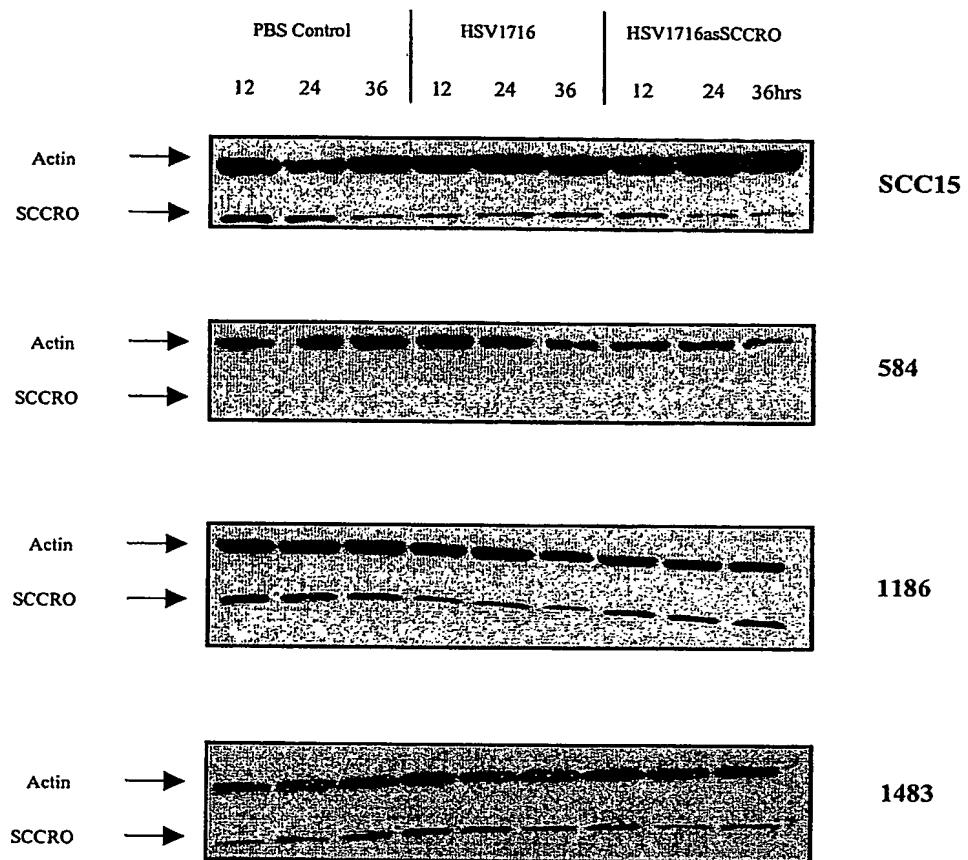
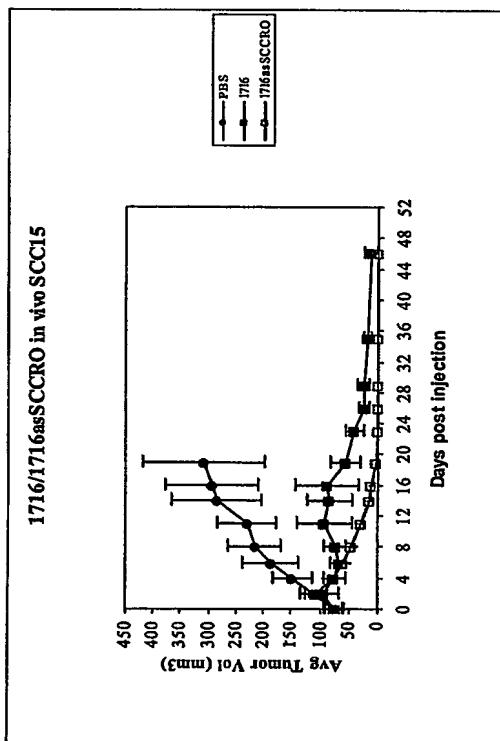
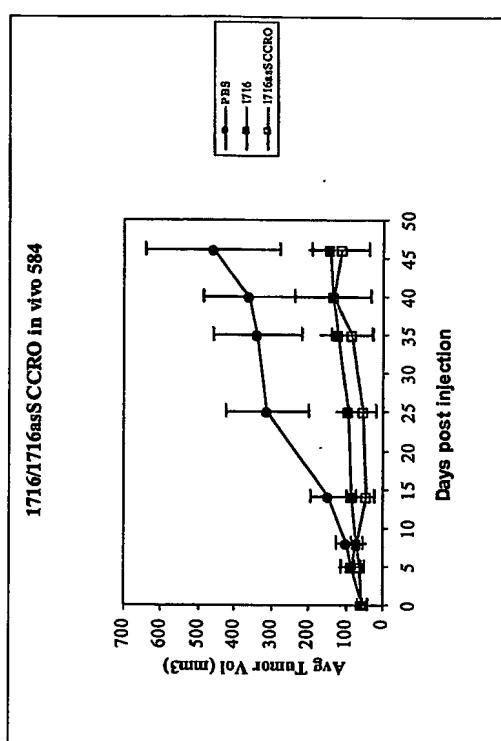


Figure 19

SCC15



584

**Figure 20**

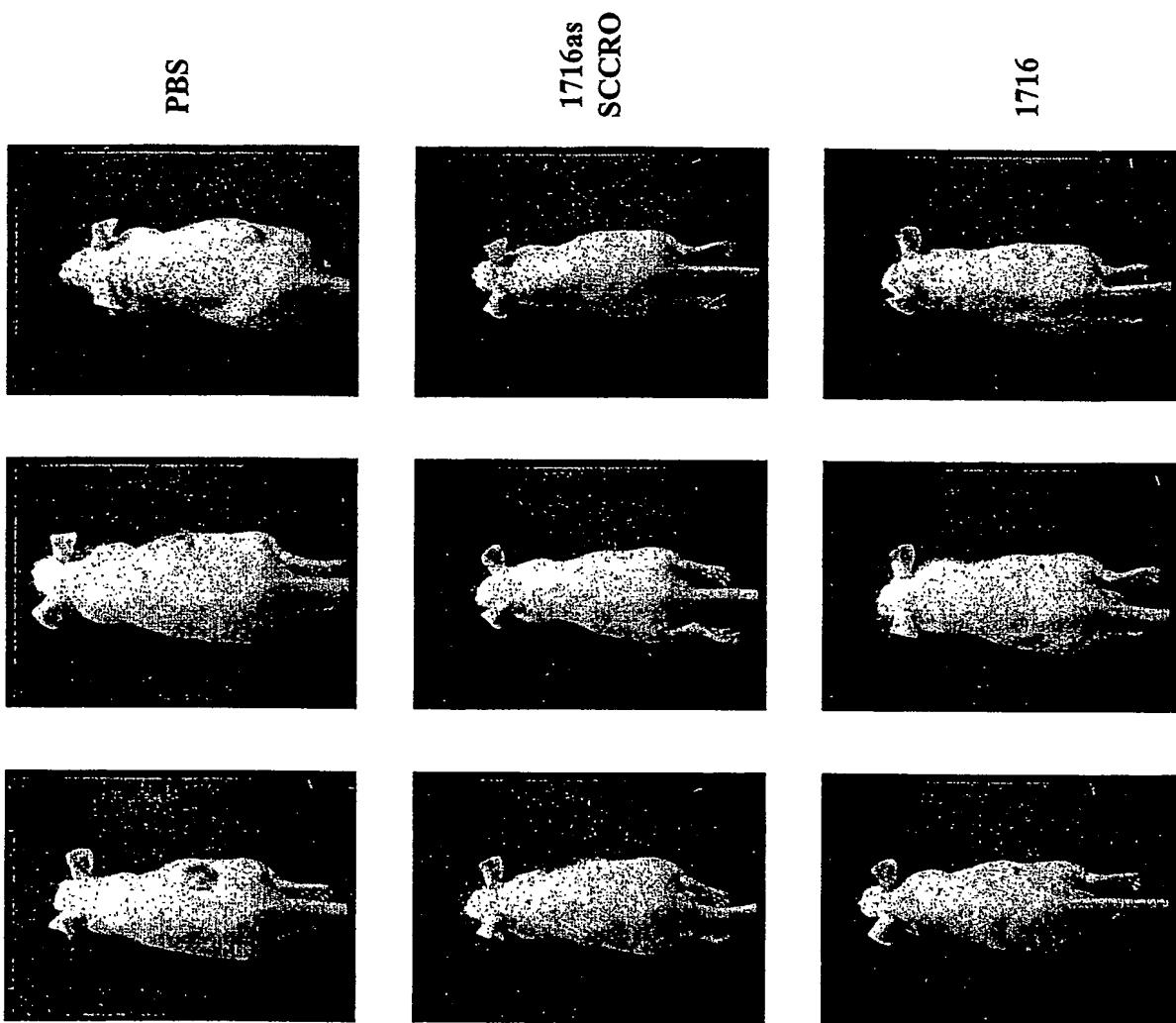


Figure 21

SEQ ID No. 01

cgcgtatc tccatggaga gacggaggag gaggggagag gatggagga cccaaac atg Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met Ile 5 10 15	60 Met I
tcc aca ttc ctt tct agt gaa aca gca gta agt tgt ctt tat cca aat Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln Asn 20 25 30	103 156
gac tgg aag tta gat gtt gca aca gat eat ttt ttc caa aat cct gaa Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro Glu 35 40 45	204
ctt tat ata cga gag agt gta eaa gga tca ttg gac agg aag aag tta Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys Leu 50 55 60 65	252
gaa cag ctg tac eat aga tac eaa gac cct caa gat gag aat aee att Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys Ile 70 75 80	300
gga ata gat ggc ate aag cag ttc tgt gat gac ctg gca ctc gat cca Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp Pro	340
gcc agc att agt gtg ttg att att gca tgg aag ttc aga gca gca aca Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala Thr 100 105 110	386
cag tgg gag ttc tcc aca cag gag ttc atg gat ggc atg acc gaa tta Gln Cys Glu Phe Ser Lys Glu Phe Met Asp Gly Met Thr Glu Leu 115 120 125	444
gga tgt gca aca ata gaa aac ata ang gcc cag ata ccc aag atg gaa Gly Cys Asp Ser Ile Glu Lys Leu Lys Ala Gln Ile Pro Iys Met Glu 130 135 140 145	492
aaa gaa ttg aac gaa cca gga cca ttt aag gat ttt taa cag ttt act Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe Thr 150 155 160	540
tct eat ttt gca aag aet cca gga cca aac gga tta gat cta gaa atg Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu Met 165 170 175	588
gac att gcc tac tgg aac tta gtg ctt eat gga aca ttt aaa ttc tta Ala Ile Ala Tyr Trp Asn Leu Leu Asn Gly Arg Phe Lys Phe Leu 180 185 190	636
gac tta tgg eat aaa ttt ttg ttt gaa cat cat eaa cga tca ate cca Asp Leu Trp Asn Lys Phe Leu Glu His His Lys Arg Ser Ile Pro 195 200 205	684
aaa gac aet tgg eat eat ctt ctt tta gac ttc agt aca atg att gca gat Lys Asp Thr Trp Asn Leu Leu Asp Phe Ser Thr Met Ile Ala Asp 210 215 220 225	732
gac atg tet eat tat eat gaa gaa gca tgg cct gtt ctt eat eat Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile Asp 230 235 240	780
gac ttt gtg gaa ttt gca cgc cct cca att gct ggg acn aca agt aca Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser Thr 245 250 255	828
aca gtg tag cactaaaggaa accttctaga atgtttatcg tctgtttatct Thr Val *	877
ccatacaca gaaaaatttca cactttt tttgtgggttg g	918

Figure 22a

SEQ ID No. 02

Met Asn Lys Ile Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met
 1 5 10 15
 Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln
 20 25 30
 Asn Asp Trp Lys Ile Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro
 35 40 45
 Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys
 50 55 60
 Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys
 65 70 75 80
 Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp
 85 90 95
 Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala
 100 105 110
 Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu
 115 120 125
 Leu Gly Cys Asp Ser Ile Glu Lys Leu Lys Ala Gln Ile Pro Lys Met
 130 135 140
 Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe
 145 150 155 160
 Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu
 165 170 175
 Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Lys Phe
 180 185 190
 Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser Ile
 195 200 205
 Pro Lys Asp Thr Trp Asn Leu Leu Asp Phe Ser Thr Met Ile Ala
 210 215 220
 Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile
 225 230 235 240
 Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser
 245 250 255
 Thr Thr Val

Figure 22b

SEQ ID No.03

Figure 22c

SEQ ID No. 04

Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met
 1 5 10 15

Ile Dhe Thr Gln Ser Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln
 20 25 30

Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro
 35 40 45

Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys
 50 55 60

Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys
 65 70 75 80

Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp
 85 90 95

Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala
 100 105 110

Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu
 115 120 125

Leu Gly Cys Asp Ser Thr Glu Lys Leu Lys Ala Gln Ile Pro Lys Met
 130 135 140

Gln Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Dhe Tyr Gln Phe
 145 150 155 160

Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Gln
 165 170 175

Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Arg Leu

Leu Asp Leu Trp Asn Lys Phe Leu Leu Gln His His Lys Arg Ser Ile
 195 200 205

Pro Lys Asp Thr Trp Asn Leu Leu Asp Phe Ser Thr Met Ile Ala
 210 215 220

Asp Asp Met Ser Asn Tyr Asp Glu Gln Gly Ala Trp Pro Val Leu Ile
 225 230 235 240

Asp Asp Phe Val Gln Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser
 245 250 255

Thr Thr Val

Figure 22d

(A) 339isiRNA (SEQ ID No. 05)

gatc**CCCGTTAGAGCAGCAACACAGTTCAAGAGACTGTGTTGCTGCTCTGAA**
CTTTTGGAAA

(B) ConisiRNA (SEQ ID No.06)

gatc**CCCCGTCTACCTACACTCCCTTTCAAGAGAGAGGGAGTAGGTAGAC**
GTTTTA

Figure 23

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